

Sub G2
E1
--Recently a polypeptide was isolated, GABA_BR1a, that binds radiolabelled GABA_B receptor antagonists in transfected cells (Kaupmann et al. 1997a). The predicted amino acid sequence, as shown in Figures 24A-24D (SEQ ID NO: 48), displays homology with the metabotropic glutamate receptor gene family which includes eight members and a Ca⁺⁺-sensing receptor. Included in this homology is a large N-terminal domain that contains two lobes with structural similarity to the amino acid binding sites of bacterial proteins. A second polypeptide, GABA_BR1b, as shown in Figures 25A-25D (SEQ ID NO: 49), presumably a splice variant, differs from GABA_BR1a in that the N-terminal 147 amino acids are replaced by 18 different residues in the predicted mature protein after signal peptide cleavage. Transcripts for both GABA_BR1s are abundant and widely distributed in the rat brain. There appear to be differences in the localization of the splice variants in discrete regions of the brain, suggesting that their expression is differentially regulated (Bischoff et al. 1997).--

On page 26, line 3, please insert the following new paragraphs:

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--**Figure 24A-24D.** Deduced amino acid sequence of the rat GABA_BR1a polypeptide (SEQ ID NO: 48).

Figure 25A-25D. Deduced amino acid sequence of the rat GABA_BR1b polypeptide (SEQ ID NO: 49).--

On page 43, line 3, please insert the following new paragraph:

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--In an embodiment of this invention, the GABA_BR1a polypeptide has an amino acid sequence identical to the amino acid sequence shown in Figures 24A-24D (SEQ ID NO: 48) and the GABA_BR1b polypeptide has an amino acid sequence identical to the amino acid sequence shown in Figures 25A-25D (SEQ ID NO: 49).--